

Fig. 1A

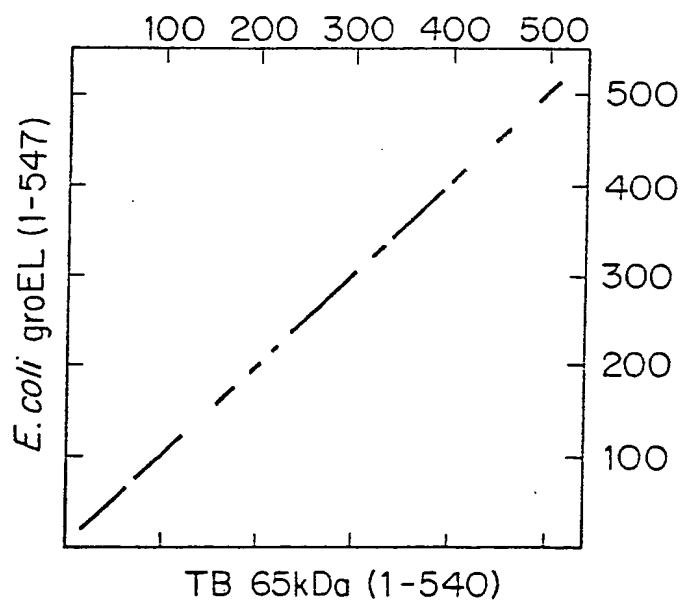


Fig. 1B

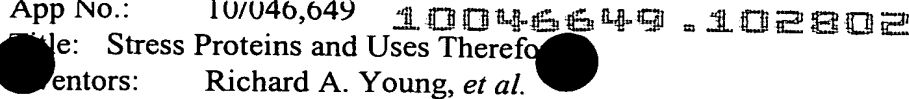


Figure 2A



421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGALLRCIPALD	SLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI					
GROEL	VEDALHATRAAVEEGVAGGVALIRVASKLADLRGQNE	DQNVVSSSL-RAMEAPLRQIVLNCGEPSVV					
491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA						
GROEL	ANTVKGGDGNYGYNAAATEEYGNMIDMGILDPTKVTR	SALQYAAASVAGLMITTECMVTDLPKND-AADLGA					
561	570						
HUMP1	MGGMGG--GMGGGNF						
GROEL	AGGMGGMGGMGGNM-						

Total score = 4667, 5 breaks
276 identities out of 545 possible matches between residues

25 random runs
Alignment score = 65.34 SD Standard deviation = 18.94 Mean = 3429.48

Figure 2B

	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKFGADARALMLQGVDDLADAVAVTMGPKGRTVTIIIEQSWGS							
ML65K	M-----AKTIAYDEEARGLERGLNSLADAVKVTLGPKGRNVVLEKKWGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLSIAKEGFEKISKGANPVEI							
ML65K	PTITNDGVSIAKEIELEDPEYKIGAEVLVKEVAKKTDVAGDGTTTATVLAQALVKEGLRNVAAGANPLGL							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE							
ML65K	KRGIEKAVDKVTETLLKDAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVIIVEESNTFFGLQ							
	211	220	230	240	250	260	270	280
HUMP1	LEIEGMKFDGRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIAEDVDG							
ML65K	LELTEGMRFDKGYISGYFVTDATERQEAQVLEEPYILLVSSKVSTVKDILLPLEKVIQAGKSLIIAEDVEG							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVLQVAVKAPGFGDNRRKNQLKDMAIATGGAVFGEGLTNLEDVQPHDLGKVGIV							
ML65K	EALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGAQVISEE-VGLTLENTDLSLLGKARKVVM							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKGGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGAVLVKVGTSDEVNEKKDR							
ML65K	TKDETTIVEGAGDTDAIAGRVAQIRTEIENSDDSDYDREKLQERLAKLAGVAVIKAGAATEVELKERKHR							

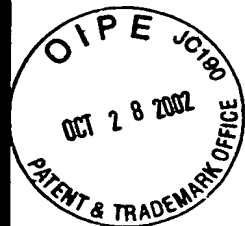
Figure 3A



421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDLSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI						
ML65K	IEDAVRNAKAAVEEGIVAGGGVTLQAAPALDKLKLTCDEAT-GANIVKVALEAPLKQIAFNSGMEPGVV						
491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA						
ML65K	AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKVTRSAQNAAAGLFTT-EAVVADKPEKTAAPASDP						
561	570						
HUMP1	MGGMGGMGGGMF						
ML65K	TGGMGG-MD---F						

Total score = 4552, 7 breaks
255 identities out of 540 possible matches between residues
25 random runs
Alignment score = 47.73 SD Standard deviation = 23.86 Mean = 3413.16

Figure 3B



1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVATMGPKGRTVIEEQSWGS						
TB65K	M-----AKTIAYDEEARGLERGLNALADAVKVTLGPKGRNVVLEKKWGA						
71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATVTLARSIAKEGFEKISKGANPVEI						
TB65K	PTITNDGVSIAKEIELEDPEYKIGAEELVKEVAKKTDVAGDGTATVLAQALRKEGLRNVAAGANPLGL						
141	150	160	170	180	190	200	210
HUMP1	RRGVM L A V D A V I A E L K K Q S K P V T T P E E I A Q V A T I S A N G D K E I G N I I S D A M K K V G R K G V I T V K D G K T L N D E						
TB65K	K R G I E K A V E K V T E T L L K G A K E V E T K E I A A T A A I S A - G D Q S I G D L I A E A M D K V G N E G V I T V E E S N T F G L Q						
211	220	230	240	250	260	270	280
HUMP1	LEIIEGKMFDRGYISPYFINTSKGQKCEFDQDAYVLLSEKKISSIQSIVPALEIANAHKPLVIAEDVDG						
TB65K	LELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLPLEKVGAGKPLLIIEAEDVEG						
281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVLQVVAVKAPGFGDNRNKQKDMAIATGGAVFGEGLTLNLEDVQPHDLGKVGIV						
TB65K	EALSTLVVNKIRGTGTFKSVAVKAPGFGDRRKAMLQDMAITGGQVISEE-VGLTLENADLSLLGKARKVVV						
351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKGGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGTSDEVNEKKDR						
TB65K	TKDETTIVEGAGDTDAIAGRVAQIRQIEIENSDDYDREKLQERLAKLAGGVAVIKAGAAATEVELKERKHR						

Figure 4A

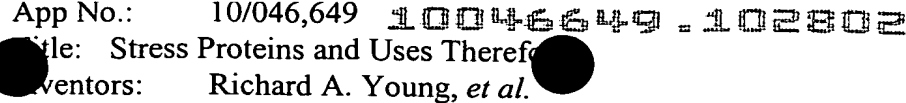


Figure 4B

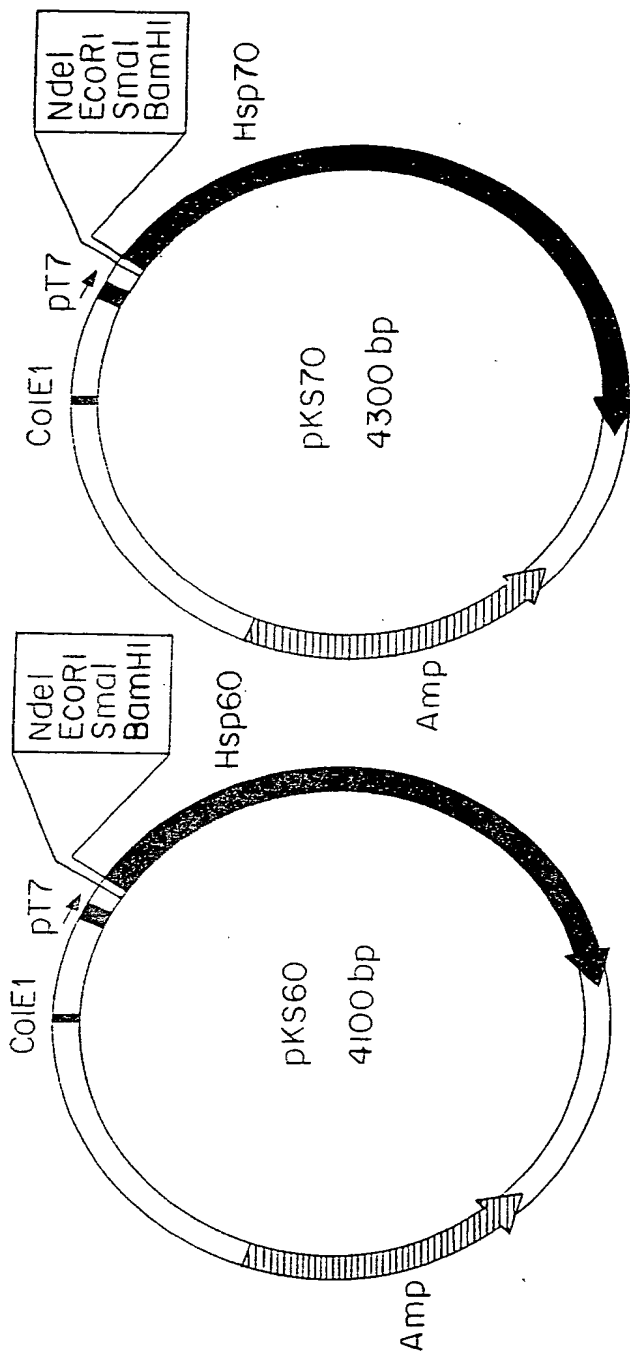


FIG. 5

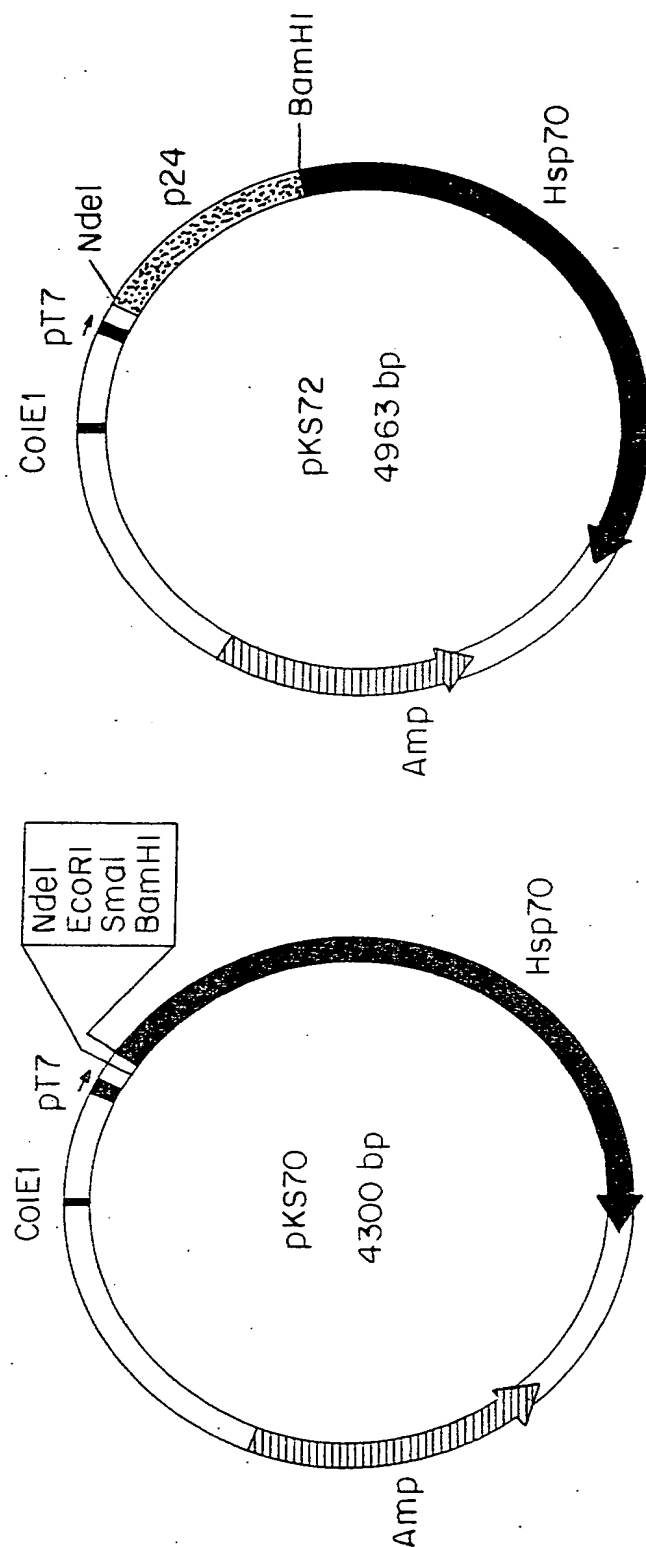


FIG. 6



App No.: 10/046,649
Title: Stress Proteins and Uses Therefor
Inventors: Richard A. Young, *et al.*

10046649 - 102802

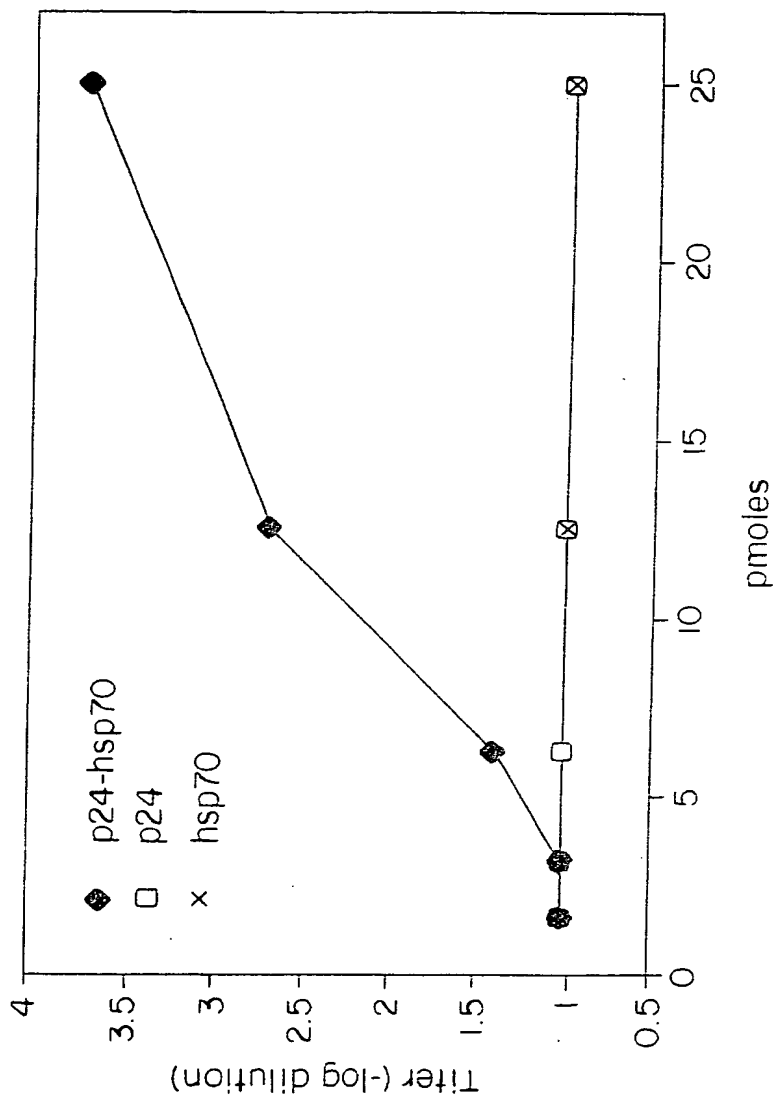


FIG. 7